

SEQUENCE LISTING

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Jurzak, Mirek

Luyten, Walter H

<120> Cloning and expression of a novel 5-HT4 receptor

<130> Novel 5HT4B splice variant

<140> PCT/EP00/05592

<141> 2000-06-14

<150> GB/9913850.5

<151> 1999-06-14

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1281

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (4)..(1209)

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15

tca gtg gag aag gtg gtg ctg ctc acg ttt ctc tcg acg gtt atc ctg 96

Ser Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu

20 25 30

atg gcc atc ttg ggg aac ctg ctg gtg atg gtg gct gtg tgc tgg gac 144

Met Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp

35 40 45

agg cag ctc agg aaa ata aaa aca aat tat ttc att gta tct ctt gct 192

Arg Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala

50 55 60

ttt gcg gat ctg ctg gtt tcg gtg ctg gtg atg ccc ttt ggt gcc att 240

Phe Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile

65 70 75

gag ctg gtt caa gac atc tgg att tat ggg gag gtg ttt tgt ctt gtt 288

Glu Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val

80 85 90 95

cgg aca tct ctg gac gtc ctg ctc aca acg gca tcg att ttt cac ctg 336

Arg Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu

100 105 110

tgc tgc att tct ctg gat agg tat tac gcc atc tgc tgc cag cct ttg 384

Cys Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu

115 120 125

gtc tat agg aac aag atg acc cct ctg cgc atc gca tta atg ctg gga 432

Val Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly

130 135 140

ggc tgc tgg gtc atc ccc acg ttt att tct ttt ctc cct ata atg caa 480

Gly Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln

145 150 155

ggc tgg aat aac att ggc ata att gat ttg gaa agg agt cta aac caa 528

Gly Trp Asn Asn Ile Gly Ile Ile Asp Leu Glu Arg Ser Leu Asn Gln

160 165 170 175

ggc ctg ggc cag gat ttt cat gcg ata gaa aag agg aag ttc aac cag 576
Gly Leu Gly Gln Asp Phe His Ala Ile Glu Lys Arg Lys Phe Asn Gln

180 185 190

aac tct aac tct acg tac tgt gtc ttc atg gtc aac aag ccc tac gcc 624
Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr Ala

195 200 205

atc acc tgc tct gtg gtg gcc ttc tac atc cca ttt ctc ctc atg gtg 672
Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met Val

210 215 220

ctg gcc tat tac cgc atc tat gtc aca gct aag gag cat gcc cat cag 720
Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His Gln

225 230 235

atc cag atg tta caa cgg gca gga gcc tcc tcc gag agc agg cct cag 768
Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro Gln

240 245 250 255

tcg gca gac cag cat agc act cat cgc atg agg aca gag acc aaa gca 816
Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys Ala

260 265 270

gcc aag acc ctg tgc atc atc atg ggt tgc ttc tgc ctc tgc tgg gca 864
Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp Ala

275 280 285

cca ttc ttt gtc acc aat att gtg gat cct ttc ata gac tac act gtc 912
Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr Val

290 295 300

cct ggg cag gtg tgg act gct ttc ctc tgg ctc ggc tat atc aat tcc 960
Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn Ser

305 310 315

ggg ttg aac cct ttt ctc tac gcc ttc ttg aat aag tct ttt aga cgt 1008
 Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg Arg
 320 325 330 335

gcc ttc ctc atc atc ctc tgc tgt gat gat gag cgc tac cga aga cct 1056
 Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro
 340 345 350

tcc att ctg ggc cag act gtc cct tgt tca acc aca acc att aat gga 1104
 Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly
 355 360 365

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 Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gln Trp Glu
 370 375 380

agt cag tgt cac ccg cca gca act tct cct ttg gtg gct gct cag ccc 1200
 Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln Pro
 385 390 395

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 Ser Asp Thr
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35 40 45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe

50 55 60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu

65 70 75 80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg

85 90 95

Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys

100 105 110

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val

115 120 125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly

130 135 140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly

145 150 155 160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Glu Arg Ser Leu Asn Gln Gly

165 170 175

Leu Gly Gln Asp Phe His Ala Ile Glu Lys Arg Lys Phe Asn Gln Asn

180 185 190

Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr Ala Ile

195 200 205

Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met Val Leu

210 215 220

Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His Gln Ile

225 230 235 240

Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro Gln Ser

245 250 255

Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys Ala Ala

260 265 270

Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp Ala Pro

275 280 285

Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr Val Pro

290 295 300

Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn Ser Gly

305 310 315 320

Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg Arg Ala

325 330 335

Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro Ser

340 345 350

Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly Ser

355 360 365

Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp Glu Ser

370 375 380

Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln Pro Ser

385 390 395 400

Asp Thr

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

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cttcatggtc aacaaggcct ac 22

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<222> (23)..(24)
<223> V = a or g or c; Y = t or c

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cccgttgtaa catctggatt tgvyggc 28

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cgcatgaaaa tcctggccca ggccttggtt 30

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<223> Y = t or c

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26

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<223> Description of Artificial Sequence: DNA primer

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